

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2002, 21:44:06 ; Search time 1920.32 Seconds

(without alignments)
2741.112 Million cell updates/sec

Title: US-09-723-970-2

Perfect score: 390

Sequence: 1 atgaagctgcattcctctt.....ccacgagctgtgagaccac 390

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estio:*
4: em_estnu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	286.2	73.4	680 9	BB624070 BB624070
2	188	48.2	405 12	AQ495547 HS-5211_B
3	176.6	45.3	560 10	BM262079 daq40d11_B
4	171.2	43.9	617 9	BE131943 daq40d11_B
5	168.2	43.1	635 10	BM262389 daq40d11_B
6	72.6	18.6	928 12	CNS0201E
7	57.8	14.8	285 12	BH327754 CH230-117
8	53	13.6	1595 11	AK017593 Mus muscu
9	50.8	13.0	592 12	BH279786 CH230-108
10	49.8	12.8	423 10	BH279786 CH230-108
11	49.8	12.8	423 10	BH279786 CH230-108
12	49.4	12.7	497 9	BE102709 UI-R-BT1-
13	48.8	12.5	434 10	BE1033915 QV2-NN200
14	48.2	12.4	372 10	BF398865 UI-R-CAL-
15	48	12.3	452 10	AV746068 AV746068
16	47.8	12.3	268 12	AZ871616 2M0184C002
17	47.8	12.3	522 9	AV173269 AV173269

18	47.8	12.3	523 9	BB618381	BB618381 BB618381
19	47.8	12.3	546 10	BF074571	BF074571 222022 MA
20	47.8	12.3	584 10	BM224915	BM224915 K0203E03-
21	47.4	12.2	584 10	BM224971	BM224971 K0204C05-
22	47.2	12.1	453 9	AI051683	AI051683 oy77h08.x
23	47.2	12.1	560 9	AV752236	AV752236 AV752236
24	47.2	12.1	678 9	AV751658	AV751658 AV751658
25	46.4	11.9	328 10	BF079065	BF079065 229583 MA
26	46.4	11.9	379 10	BF442180	BF442180 258778 MA
27	46.4	11.9	409 10	BE749737	BE749737 200773 MA
28	46.4	11.9	414 10	BF075383	BF075383 224374 MA
29	46.4	11.9	476 10	BF442020	BF442020 258543 MA
30	46.4	11.9	482 10	BF080835	BF080835 231861 MA
31	46.4	11.9	515 10	BI343866	BI343866 372161 MA
32	46.4	11.9	516 10	BI345127	BI345127 373848 MA
33	46.4	11.9	527 10	BF02350	BF02350 MI-P-A2-a
34	46.4	11.9	527 10	BI339266	BI339266 364172 MA
35	46.4	11.9	625 9	AV753384	AV753384 AV753384
36	45.8	11.7	634 9	AV745740	AV745740 AV745740
37	45.4	11.6	481 9	AI189453	AI189453 qd02c08.x
38	45.4	11.6	525 9	AI148695	AI148695 qc58904.x
39	45	11.5	544 9	AI148647	AI148647 qc69a08.x
40	44.8	11.5	519 9	AI149163	AI149163 qc76a04.x
41	44.6	11.4	447 9	AI291937	AI291937 qm81c01.x
42	44	11.3	437 9	AV748886	AV748886 AV748886
43	44	11.3	487 10	BF190158	BF190158 236616 MA
44	44	11.3	539 9	AI188964	AI188964 qd22B08.x
45	43.8	11.2	446 9	AI276216	AI276216 q176b05.x

ALIGNMENTS

RESULT 1
LOCUS BB624070
DEFINITION BB624070 RIKEN full-length enriched, adult male eyeball Mus musculus CDNA clone 7530426119 5', mRNA sequence.
ACCESSION BB624070
VERSION BB624070.1 GI:16462680
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M., and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Wegli,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A., and Hayashizaki,Y.

TITLE JOURNAL COMMENT


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/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/notes="Vector: pRT3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pRT3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery'. Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-d18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pRT3-Pac vector.
The library contained approximately 7.2 x 105
recombinants, with average insert sizes of 1-1.5 kb."
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BASE COUNT 189 a 139 c 151 g 138 t

ORIGIN

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Query Match 43.9%; Score 171.2; DB 9; Length 617;
Best Local Similarity 67.9%; Pred No. 2.6e-33;
Matches 239; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 30 catggccctcctctctgctgctatgctgctcctcctcagtggaacct 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 266 CCGCAGCTTCGTGGTTTGGCCCTGTCTCAGACCGCTGCAGATCCATATATAGTCT 325

QY 90 ggcacacttctggtgctgctgctgaggaagttacttctcggccaagaagcagctg 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 326 GAGAACGTTCAATGGATGTCGTGTGAGGAAATTCATCTTAAGCAAAACCTGGCTG 385

QY 150 caggggcctcctgatacacaagatcctcctgctgctgctggaacctggaagaacc 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 386 CAGAGGTCGCGGTGACACTGATGCTGCTGGGGCCCTGTGAGACCTGTGAGAGGCC 445

QY 210 cactctggaacccccctatatattgaagcccatcagatcctctactacaagaagca 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 446 ATCCCTAGATCCCTCCCTACATAGAACCCACAGAGCTCTGACATTAATGAATCTAA 505

QY 270 acaagtgactgtcaagctcccaactgtgcccggagagtcgaccccttaccactatcc 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 506 ACTGGTTACTGTATATCTGCAAACTGCAAGCCAGACATTGACCCATTCTTTACTACCTACC 565

QY 330 cgtggccatccgctgtgactgctgagagcctgctcactgccaacgagagtg 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 566 AGTTGCCATTAGATGTGACTGTGACATGTGTCCACTTCTACTACGAATATGT 617

RESULT 5
LOCUS BM62389 635 bp mRNA linear EST 18-DEC-2001
DEFINITION da940d11.v3 Blackshear/Soares normalized Xenopus egg library
Xenopus laevis cDNA clone IMAGE:4783917 5' similar to SW:GTHA_CTFCA
P01235 GONADOTROPIN BETA CHAIN PRECURSOR. [1] ; mRNA sequence.
ACCESSION BM62389
VERSION BM62389.1 GI:17925429
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 635)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martini, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
, B., Gibbons, M., Harvey, N., Rifter, E., Jackson, Y., McCann, R.,
Washu Xenopus EST project, 1999
Washtu Xenopus EST project, 1999
TITLE JOURNAL
COMMENT Other_ESTS: da940d11.x3
Contact: Sandy Clifton, Ph.D.
```

Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo
(University of Iowa). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/BLNL at: info@image.llnl.gov
Seq primer: -40RP from Glibco
High quality sequence stop: 491.
Location/Qualifiers

FEATURES
source
1..635
/organism="Xenopus laevis"
/db_xref="taxon:9355"
/clone_image="4783917"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"

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BASE COUNT 187 a 153 c 153 g 142 t
ORIGIN
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Query Match 43.1%; Score 168.2; DB 10; Length 635;
Best Local Similarity 68.3%; Pred No. 1.5e-32;
Matches 233; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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QY 30 catggccctcctcctctctgctgctatgctgctcctcctcagtggaacct 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 295 CCGCAGCTTCGTGGTTTGGCCCTGTCTCAGACCGCTGCAGATCCATATATAGTCT 354

QY 90 ggcacacttctggtgctgctgctgaggaagttacttctcggccaagaagcagctg 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 355 GAGAACGTTCAATGGATGTCGTGTGAGGAAATTCATCTTAAGCAAAACCTGGCTG 414

QY 150 caggggcctcctgatacacaagatcctcctgctgctgctggaacctggaagaacc 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 415 CAGAGGTCGCGGTGACACTGATGCTGCTGGGGCCCTGTGAGACCTGTGAGAGGCC 474

QY 210 cactctggaacccccctatatattgaagcccatcagatcctctactacaagaagca 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 475 ATCCCTAGATCCCTCCCTACATAGAACCCACAGAGCTCTGACATTAATGAATCTAA 534

QY 270 acaagtgactgtcaagctcccaactgtgcccggagagtcgaccccttaccactatcc 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 535 ACTGGTTACTGTAAACTGCAAACTGCAAGCCAGACATTGACCCATTCTTTACTACCTACC 594

QY 330 cgtggccatccgctgtgactgctgagagcctgctcactgccaacgagagtg 370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 595 AGTTGCCATTAGATGTGACTGTGACATTTGTTCCACTTCTTA 635

RESULT 6
LOCUS CNS0201E 928 bp DNA linear GSS 14-MAY-2000
```

TITLE	A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.		
JOURNAL	Rat BAC End Sequences from Library CHORI-230 EcoRI segment unpublished (1999)		
COMMENT	Other_GSSs: CH230-117A17.TJ Contact: Shaying Zhao Department of Eukaryotic genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering/information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 117 row: A column: 17 Seq primer: T7 Class: BAC ends.		
FEATURES	Location/Qualifiers		
source	1..285		
	/organism="Rattus norvegicus"		
	/strain="BN/SSNHsd/MCW"		
	/db_xref="taxon:10116"		
	/clone="CH230-117A17"		
	/clone_1lb="CHORI-230 Segment 1"		
	/sex="Female"		
	/cell_type="Brain"		
	/note="Vector: PTARBAC2.1, Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pletier de Jong"		
BASE COUNT	60 a 66 c 83 g 76 t		
ORIGIN			
Query Match	14.8%, Score 57.8; DB 12; Length 285;		
Best Local Similarity	96.7%; Pred. No. 0.00013;		
Matches	59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
OY	144 aggcgcagggggcccttgatcacacgagatgctgcgcgggggtgcgttgagacttgga 203		
Db	1 AGCGCGCAGGGGACTTCGATCACCACGACGATGCCGTGGGGGTGCGTGGAGACTTGGA 60		
OY	204 g 204		
Db	61 G 61		
RESULT	8		
AK017593	LOCUS		
DEFINITION	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730420N04;follicle stimulating hormone beta, full insert sequence.		
ACCESSION	AK017593		
VERSION	AK017593.1 GI:12856911		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (Strain:C57BL/6J) 8 days embryo cDNA to mRNA, clone_1lb:RIKEN full-length enriched mouse cDNA library clone:5730420N04.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (sites)		
REFERENCE	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
REFERENCE	99279253		
REFERENCE	10349636		
REFERENCE	2 (sites)		
REFERENCE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,		


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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B71-4q-p-11-0-UI"
/clone_lib="UI-R-B71"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pRTT3D-Pac (pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The library
UI-R-B71 is a subtracted library derived from a mixture o
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
rateest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-B71
TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"

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	Query Match	Similarity	12.8%	Score 49.8	DB 9	Length 497
	Best Local	Similarity	55.5%	Pred No. 0	016	Indels 0
	Matches	96	Conservative	0	Mismatches 77	Gaps 0
OY	212	tctctggaaccccccttatatgaaagcccaatcatgatgtctgtacctacaagaaccacaac	271			
Db	332	TACTCGACAGCTGCCTTGCTCCCGTGTGTCAGGCAAGTAGACACTTAACGGTAGCTGGCT	273			
OY	272	aggtagtcgtcaagtctggccaactgtgcccgvgagtgaaaccttctacattcccg	331			
Db	272	TGCGCCTGTCTCCGCCCTCCCTGGCTGGCCACATGCTGTAAAGCCCCCAAGTCTCCTTTCTCTG	213			
OY	332	tggcgcatacgcgtgtgactcggagaccctgtctcaactcgcccacaaggagatgtgag	384			
Db	212	TGGCCCTCACACTGCCCCTGTGGGCCCTTCCCGCTTCACGTAGCTTGTGACTGTGGG	160			

RESULT	12
BIO33915/C	
LOCUS	
DEFINITION	Ovz-NN20004 -080301-614-f05 NN2004 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BIO33915
VERSION	BIO33915.1 GI:14440541
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo. 1 (bases 1 to 434)
AUTHORS	Dias Neto, E., da Silva, W. Jr., Zagdo, M.A., Bordin, S., Costa, F.F., Nagdi, A.V., de Almeida, R., Verjowski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsushima, A., Baía, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, W.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.U.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL MEDLINE COMMENT	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
Contact:	Simpson A.U.G.
Laboratory of Cancer Genetics	
Ludwig Institute for Cancer Research	
Rua Prof. Antonio Prudente 109, 4 andar,	01509-010, Sao Paulo-SP, Brazil
Tel.: +55-11-2704922	
Fax: +55-11-2707001	
Email: asimpson@ludwig.org.br	
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project.	This entry can be seen in the following URL

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FEATURES
source
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl-QV2&t2-QV2-NN2004
080301-614-f05&f3=2001-03-08&f4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
Location/Qualifiers
1..434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN2004"
/dev_string="Adult"
Note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
transfected into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
107 a 102 c 108 g 117 t

```

	Query Match	Score	DB	Length
Best Local Similarity	54.2%	Pred. No. 0.02;		
Matches	123;	Conservative	0;	Mismatches 101; Indels 3; Gaps 1;
OY	155	gccttcgcatcaaccagcgcctcgtcgtggtgcgtctgtgagacctcgtggagaaaccatc	214	
Db	302	GCATTAAGATCAACACCACTTCTGTGCTGCTACTGCATCACCGAGGCTTCGTGTATA	243	
OY	215	tggaaacccccctatatgtgaagccatcatcgcgtctgtatccctacaaagcagaccacag	274	
Db	242	AGGACCCAGCCAGGCTCAAGATCCAGAACACA---TGTACCTTCAGAGCAACTGGTATAG	186	
OY	275	tgcactgcaagctgcgccaaactgtgcgccggagatgcgacccctctacacctatcccgty	334	
Db	185	AAACAGTGAAGATGCCCGCTGTGCTCAACATGCAAGATCTTGTATACATACCCAGTG	126	
OY	335	ccatccgcgtgtgactgcgcgagcctgtctccactgcacacccaggaagyt	381	
Db	125	CCACCAGTGTCACTGTGTGGCAAGTGAAGCGACAGCACTATTGT	79	

[illegible]


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/db_xref="taxon:9606"
/clone="TPAEH04"
/clone_lib="TP"
/tissue_type="pituitary tumor"
/dev_stage="Adult"
/lab_host="BM25.8"
/Note="Vector: pT19plex2; Site_1: sflIA; Site_2: sflIB"

BASE COUNT      156 a      143 c      156 g      149 t      2 others
ORIGIN

Query Match      12.5%; Score 48.8; DB 9; Length 606;
Best Local Similarity 60.6%; Pred. No. 0.031;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 230  tgcctcaacgagacacaacaggtgactgctgcaagctgcccgaactgtgccccggagatc 309
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 207  TGTACTCTCAAGAGACTGGTATATGAACAGAGAGAGCCGCGCTGTGCTCACCATGCA 266
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 310  gaccctcttaacctatcccgctgcaatccgctgtgactgctggagagcctgtctcactgcc 369
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 267  GATTCCTGTATACATACCCAGTGGCCACCCAGTGTCACTGTGGCAGTGTGACAGCGAC 326
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 370  accacgagatgt 381
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 327  AGCACTGATGTGT 338
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
LOCUS BP398865/c
DEFINITION UT-R-CA1-bJ-a-a-15-0-UI.s1 UT-R-CA1 Rattus norvegicus cDNA clone
ACCESSION BF398865
VERSION BF398865
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 372)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704447
JOURNAL CONTACT: Soares, MB
MEDLINE Program for Rat Gene Discovery and Mapping
COMMENT University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mssoares@blue.weeg.iowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized corpus-striatum library cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.

FEATURES
SOURCE
1..372
Location/Qualifiers
1..372
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA1-bJ-a-a-15-0-UI"
/clone_lib="UI-R-CA1"
/lab_host="DH10B (Life Technologies)"
/Note="Vector: pT19T3D-Pac (Pharmacia) with a modified

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polylinker site.1: Not I; Site.2: Eco RI; The UI-R-CAL library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratel.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_LIB=UI-R-CAL
TAG_TISSUE=cortex-striatum
TAG_SEQ=CCTAGC"

BASE COUNT 88 a 75 c 138 g 71 t

ORIGIN

Query Match 12.4%; Score 48.2; DB 10; Length 372;
Best Local Similarity 54.9%; Pred. No. 0.038;
Matches 95; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Oy 212 ttcttgaaacccccatatltgaagccatcgcgtgtaacttaccatacaaggacaac 271
 | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 332 TACTCCAGCATGTCATGTGGCTCCCGGCCCTACACCAGTGTGACCTACGCTGCGCT 273
 | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 272 aggtgcatcgtaaacgtgcccaactgtggcccggaggtgcacctttacactaccg 331
 | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 272 TGCGCTCTGTGCCTCCCTCCCTGCCCCACCGTGGTGAGACCCCAATTGCTCTTCTCG 213
 | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 332 tggccatccgtctgtagtcgtgcagcctctcacacgcaccacagagtgtgag 384
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Db 212 TTGGCCCTCAGCTGCGCGCTGTGGGCCCTCCGCTCCTCAGTACGCTTACTGTGGG 160
 | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
AV746068 452 bp mRNA linear EST 18-OCT-2000
LOCUS AV746068
DEFINITION AV746068 NPA Homo sapiens cDNA clone NPADL10 5', mRNA sequence.
ACCESSION AV746068
VERSION AV746068.1 GI:10865515
KEYWORDS EST.

SOURCE
ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 452)
 Song,H., Peng,Y., Gu,X., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Gu,
 Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,
 W., Tu,X., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.
 Han,Z., Chen,Z., Hu,R. and Chen,J.
 Homo sapiens NPA library CDNA clones
 Unpublished (2000)
CONTACT Shanghai Institute of Endocrinology, Rui-jin Hospital
 Contact: Qinghua Zhang
 Shanghai National Human Genome Center at Shanghai
 197 Rui-jin II Road, Shanghai 200023, P. R. China
 Tel.: 86-21-64370045(ex.663332)
 Fax: 86-21-64743206
 Email: mbsheims.stn.sh.cn
 This clone is available at Shanghai Hematology Institute in
 Shanghai.
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
LOCATION/Qualifiers
 1..452
FEATURES
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NPADL10"
 /clone_id="NPA"
 /tissue_type="pituitary"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

PAGE COUNT 58 a 177 c 122 g 91 t 4 others

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2002, 21:21:20 ; Search time 1723.48 Seconds
(without alignments)
4735.390 Million cell updates/sec

Title: US-09-723-970-2

Perfect score: 390
Sequence: 1 atgaagctggcattctctt.....ccacgagtgtagacacac 390

Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_pi:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description
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1	390	100.0	390	6	AX259341	AX259341 Sequence
2	390	100.0	917	6	AX201855	AX201855 Sequence
3	378	96.9	693	6	AX193583	AX193583 Sequence
4	300.4	77.0	393	6	AX259351	AX259351 Sequence
5	252	64.6	1045	9	AX201857	AX201857 Sequence
6	204	52.3	12252	9	CNS01DKS	AL118553 Human chr
7	202	51.8	205	6	AX193608	AX193608 Sequence
8	192	49.2	169650	9	CNS0000U	AL049871 Human chr
9	156	40.0	2985	6	AX259362	AX259362 Sequence
10	69	17.7	1060	5	ASPT251658	AJ251658 Acipenser
11	66.4	17.0	687	5	SCA310345	AJ310345 Scyllorhin
12	61.6	15.8	406	6	108476	108476 Sequence 16
13	61.6	15.8	504	4	CEFLHR	Y00518 Dog mRNA fo
14	61.6	15.8	579	4	AY056475	AY056475 Monodelph
15	61	15.6	426	6	108475	108475 Sequence 14
16	60.8	15.6	580	5	ASPT251656	AJ251656 Acipenser
17	59.2	15.2	558	5	CIGCONADB	X61051 C. iodeila mr
18	59.2	15.2	566	5	AF319960	AF319960 Mylrophary
19	58.4	15.0	429	4	AF354938	AF354938 Panthera
20	58.4	15.0	448	5	FUNCTHIT	M87015 Fundulus he
21	57.8	14.8	525	6	A06106	A06106 Synthetic p
22	57.8	14.8	629	4	BOVLHBB	M10077 Bovine lutr
23	57.4	14.7	2309	5	AB015596	AB015596 Carassius
24	56.8	14.6	535	5	D88024	D88024 Carassius a
25	56.8	14.6	5651	6	AX211282	AX211282 Sequence
26	56.8	14.6	5651	6	AX349366	AX349366 Sequence
27	56	14.4	426	6	E01778	E01778 DNA Sequence
28	56	14.4	581	5	AF112192	AF112192 Ictalurus
29	56	14.4	661	5	ONHSTHIB	M27154 Chum salmon
30	56	14.4	999	5	RR131135	AJ311355 Rana ridl
31	56	14.4	1864	4	BOVLHBB	AJ11506 Bovine lute
32	55.6	14.3	585	4	AF090388	AF090388 Trichosur
33	55.6	14.3	601	4	AF017448	AF017448 Trichosur
34	55.6	14.3	789	5	AF112191	AF112191 Ictalurus
35	55.6	14.3	875	5	ONHRTBS	D14692 Rainbow tto
36	54.8	14.1	395	5	AHA417769	AJ417769 Atlantic
37	54.6	14.0	527	5	CHGTHIB	X91984 C. harengus
38	54.6	14.0	533	5	OALHBS	AB050836 Oncorhyn
39	54.4	13.9	659	5	AB050836	AB050836 Cyprinoceph
40	54.4	13.9	1054	9	AF397610	AF397610 Cyprinoceph
41	54.2	13.9	590	5	MOZCONAIB	L35096 Morone sax
42	54	13.8	810	5	CCO271632	AJ271632 Conger co
43	54	13.8	866	5	AF060566	AF060566 Salmo sal
44	54	13.8	1066	5	AB016169	AB016169 Anguilla
45	53.6	13.7	426	4	AF448455	AF448455 Alluoropod

ALIGNMENTS

RESULT 1
AX259341
LOCUS AX259341 390 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 2 from Patent WO01/3034.
ACCESSION AX259341
VERSION AX259341.1 GI:16508575
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Pastzy,C.J., Cao,J., Danilenko,D.M., Gong,J. and Hill,D.C.
TITLE Beta-like glycoprotein hormone polypeptide and heterodimer
JOURNAL Patent: WO 01/3034-A 2 04-OCT-2001;
Amgen Inc. (US)
Location/Qualifiers

FEATURES
source 1..390
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 69 a 128 c 106 g 87 t
ORIGIN

Query Match	100.0%;	Score 390;	DB 6;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 5.5e-87;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 atgaagcttgacatccctccctcccttgagcccaatggccccctccctcttgatgctatggc 60
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Db 1 atgaagctggcattccctcttcccttgagcccccacatggccccctccctcttgatgctatggc 60

Dy 61 tggtagcctcggtgctccacagtgaggaaacctgcgacacttcttgagcgtgtgcgltgagggag 120
|||
Db 61 TGTGTCCTGGGTGCCCTCCAGTGGGAACCTGCACCTTTGTGGCGTGTCGCCGTAGAAGGAG 120

121 tttaacttcctcgcgaagaagccagctgcgagggcccttcgcgatccaccagcgatgcctgc 180
 121 tttacttcttcctggcccaagaagccagcctgcagggggccttcggatcaccacgagtcctgc 180

181 TGGGGTCGCTGTGAGACCTGGGAGAAACCCATTCTGGAACCCCTATATTGAAGCCCAT 240

Db 241 CACGAGTGTCTACTACAACGAGACCAACAGTGACTGTCAAGCTGCCAACCTGGCC 300

301 CCGGGAGTCGACCCCTTCTACACCTATCCCGGGCCATCCGCTGACTCGGAGCCCTGC 360

Db 361 TCCACTGCCACACGAGTGTGAGACCATC 390

LOCUS	AX201855	917 bp	DNA	linear	PAT 30-AUG-2001
RESULT 2	AX201855				

ACCESSION AX201855
VERSION AX201855.1
KEYWORDS GI:15391696
*
burns
cornea

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 917)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

AUTHORS Mosselman, S. and Spek van der, P.J.
TITLE Human cystine knot polypeptide
JOURNAL Patent: WO 0153346-A 1 26-JUL-2001;
Akzo Nobel N.V. (NL)

```

FEATURES
SOURCE
LOCATION/Qualifiers
1. 917
/organism="Homo sapiens"
/db_xref="taxon:9606"

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ORIGIN	2003	2004	2005	2006	2007
INDIA	24.1	24.0	24.0	24.0	24.0
CHINA	23.9	23.9	23.9	23.9	23.9
USA	23.8	23.8	23.8	23.8	23.8
EUROPE	23.7	23.7	23.7	23.7	23.7
AFRICA	23.6	23.6	23.6	23.6	23.6
ASIA	23.5	23.5	23.5	23.5	23.5
AMERICA	23.4	23.4	23.4	23.4	23.4
AUSTRALIA	23.3	23.3	23.3	23.3	23.3
NEW ZEALAND	23.2	23.2	23.2	23.2	23.2
OTHER	23.1	23.1	23.1	23.1	23.1

Best Local Similarity 100.0%; Pred. No. 5.1e-87;
Matches 390; Conservative 0; Mismatches 0; Indels 0;
Gaps 0

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Db 161 TGTCTCTCGGTGCCCTCCAGTGGGAACCTGGCACACTTTGTGGCCTGTGCCGTGAGGGAG 220

Db 221 TTACTTCTCGGCCAGAGCCAGGCTGCAGGGCCCTTCGATCACCACGAGATGCCCTGC 280

Qy 181 tggagtcgctgtgagacctgggagaaacccatcttgaaacccctatatitgaagccat 240
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Db 281 TGGGTCGCGCTGAGACCTGGGAGAAACCATCTCTGAAACCCCTATATTTGAAGCCCAT 340
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|||

[illegible]

QY 301 ccgagagtgcacccctctcaacctatcccgtgscatccgcgtgtgactcgcgagactgc 360
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Ddb 401 CCGGAGTGCACCCCTTTACAACCTATCCGGTGCCATCCGCTGTGACTCGGAGCCTGC 460

[illegible]

RESULT	3				
AX193583					
LOCUS					
AY193583					
	693 bp	DNA	linear	pat	15-ATC

DEFINITION	Sequence 5 from patent WO140231.
ACCESSION	AX193583
VERSION	AX193583.1
KEYWORDS	GI:15211515

ORGANISM	Homio sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	

AUTHORS	TITLE
Burgess, C.E., Prayaga, S.K., Shinkets, R.A., Rastell, L., Zernhusen, B.D. and Mezes, P.S.	Proteins and nucleic acids encoding the same

Curagen Corporation (US)	
Location/Qualifiers	
1. .693	

	/db_xref="taxon:9606"			
BASE COUNT	138 a	197 c	196 g	162 t
ORIGIN				

Query Match	96.9%;	Score 378;	DB 6;	Length 693;
Best Local Similarity	100.0%;	Pred. No. 5.1e-84;		
Matches 378:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 atgaagctgcatctcctctcttgccacatgagccctcctcctctgctgcatgac 60
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1 ATGAAGCTGCGCATCTCCTCTCTTGCCACATGAGCCCTCCTCCTGCTGCGCATGAC 60

QY 61 tgtgtcctcggatgctcccaagtgggaacctgacgaccttctgtggcgtgtgccgtgaggag 120
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Db 61 TGTGTCCTCGGATGCTCCCAAGTGGGAACCTGACGACCTTCTGTGGCGTGTGCCGTGAGGAG 120
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QY 121 tttaacttcctgccaagaagccagcctgcagagggccttcgataccacagatgcctc 180
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Db 121 ttttaacttttccgagcccaagaagccagggccttcgataccacagatgcctc 180
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QY 181 tggggtcgtctgtgagacctgggagaaccatctctggaacccccctatatitgaagccat 240
|||||
Db 181 TGGGGTCGCTGTGAGACCTGGGAGAACCCATCTGGAACCCCCCTATATTTGAAGCCAT 240

QY 241 catcgagtcgtactacaagagacaacagtgactgaagctgcccactgtgcc 300
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Db 241 CATCAGTCTGTACCTACACAGAGACCAACAGGTGACTGTCAAAGCTGCCAAGTGTGCC 300

Qy 301 ccggagagtcgacccctctacacataccgctgycalcgcgtgtgactcgagacgtgc 360
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Db 301 ccggagagtcgacccctcttctacacataccgctgycalcgcgtgtgactcgagacgtgc 360

0y 361 tccactgcccaccacgag 378
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[illegible]

TITLE	Human cystine knot polypeptide
JOURNAL	Patent: WO 0153346-A 3 26-JUL-2001;
FEATURES	Akzo Nobel N.V. (NL)
SOURCE	Location/Qualifiers 1..1045
BASE COUNT	254 a 279 c 234 g 278 t
ORIGIN	

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Query Match          64.6%; Score 252; DB 6; Length 1045;
Best Local Similarity 75.3%; Pred. No. 1.2e-52;
Matches 390; Conservative 0; Mismatches 0; Indels 128; Gaps 1;

OY      1 atgaagctgcatcctccctcctcttgcccacatggccctccctcctctgtgctgatatgc 60
DB     101 ATGAAGCTGGGCAATTCCTCTTCTTGCCCCAATGGCCCTCCTCCTTGCGGTGGCATGGC 160
OY      61 tglgtcctcgatgctcccaagtggagaacctgcgcacttltgtggagctgtgccgttagaggag 120
DB     161 TGTGTCCTCGGGGCTCCACGTGGGAACCTGCACACTTTGTTGGGCTGTGCCGTGAGGAG 220
OY     121 tttaatttcctggccaagaaccagagctgcagagggccttgtgatcacagagatgacctgc 180
DB     221 TTTAATTTCCTGGCCCAAGAAGCCAGGCTGCAGAGGGGCTTGGGATCACACGAGATGCCCTGC 280
OY     181 tggagctgcctgtgaacctgtggag----- 204
DB     281 TGGGGTCCGCTGTGAGAACCTGGGAGCTTTTGTCAGATGTGCTGTATGAACAAGCATTCGA 340
OY     205 ----- 204
DB     341 ATACACATTTGTTGGTGTGACTGGATGAGACCTCCCCTCGAGAGCTGTAGATCCTCCAGCCT 400
OY     205 -----aaaccatcttggaaecceccataatgt 232
DB     401 AATGGAAAGGCATTGTAGATCACACTTGCACCTAAACCATTCTGGAAACCCCTATATATGG 460
OY     233 aaagccatcatcagatgctctgtaacctacaacagagaccaagatgacttcaagctgtgcca 292
DB     461 AAAGCCATCATTCAGACTGTGTACTCTCAACGAGAACCAACAGTAGTCTCAAGCTGCCCCA 520
OY     293 actgtgccccggagatgcgaacctctacaactatcccggtggcaatccgctgtgactgcg 352
DB     521 ACTGTGCCCCGGGAATGCAGCCCTCTCTACACTTATCCCGTGGCAATCCGCTGTGACTGCG 580
OY     353 gagcctgtctcaactgagccaacagagatgtgagaccatc 390
DB     581 GAGCCTGTCTCCACTGCCACACAGGAGTGTGAGACCATC 618

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RESULT 6

CNSOLIDS	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
CNSOLIDS	LOCUS	Human chromosome 14 DNA sequence BAC C-2011M8 of library Caltech-D from chromosome 14 of Homo sapiens (Human), complete sequence.	AL118555		HTG.	human.
ORGANISM		Homo sapiens				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE		1 (bases 1 to 122552)				Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Winkler,P., Brodier,P., Calciolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Guyon,G., Saurin,W. and Weissbach,J.
AUTHORS		Sequencing of the human chromosome 14 unpublished				2 (bases 1 to 122552) Genoscope.

Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-111J20
Downstream BAC (overlapping the SP6 end) : C-2011M8 (AC-AL118555)

Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.69x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases

1 - 9 :
10 - 19 :
20 - 29 :
30 - 39 :
40 - 49 :
50 - 59 :
60 - 69 :
70 - 79 :
80 - 89 :
90 - 99 :
112230

Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

SOURCE

1. 169650

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/clone="R-696D21"

/clone_lib="RPCI-11"

79560..79769

/note="matching EMBL:G11018"

RHdb:RH35164

dbSTS:STS8422

Identified using the e-PCR software (G. Schuler)"

123442..123577

RHdb:RH77820

dbSTS:STS54362

Identified using the e-PCR software (G. Schuler)"

124823..124920

/note="matching EMBL:AA011182"

RHdb:RH75585

dbSTS:STS52673

Identified using the e-PCR software (G. Schuler)"

125981..126128

/note="matching EMBL:N67960"

RHdb:RH65935

dbSTS:STS45865

Identified using the e-PCR software (G. Schuler)"

52841 a 35988 c 32593 g 48428 t

BASE COUNT

ORIGIN

Query Match 49.2% Score 192; DB 9; Length 169650;
Best Local Similarity 99.5% Pred. No. 7.3e-38;
Matches 203; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 atgaagctggacattcctctctggcccaatggccctcctctctgctgctatgac 60

Db 150808 ATGAAGCTGGACATTCCTCTCTGGCCCAATGGCCCTCCTCTCTGCTGCTATGAC 150749

QY 61 tctgtccctcgtgtcctccagtggaacctgtgcaccttctgtggtcgtgtcgtgagga 120

RESULT 9
AX259362 2985 bp DNA linear PAT 26-OCT-2001

LOCUS AX259362

DEFINITION Sequence 23 from Patent WO0173034.

ACCESSION AX259362

VERSION AX259362.1 GI:16508593

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (stiles)

AUTHORS Paszty,C.J., Cao,J., Danilenko,D.M., Gong,J. and Hill,D.C.

TITLE Beta-like glycoprotein hormone polypeptide and heterodimer

JOURNAL Patent: WO 0173034-A 23 04-OCT-2001;

Amgen Inc. (US)

FEATURES

SOURCE

1. 2985

/organism="Mus musculus"

/db_xref="taxon:10090"

BASE COUNT 784 a 630 c 761 g 810 t

ORIGIN

Query Match 40.0% Score 156; DB 6; Length 2985;

Best Local Similarity 85.3% Pred. No. 9.6e-29;

Matches 174; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 atgaagctggacattcctctctggcccaatggccctcctctctgctgctatgac 60

Db 1 ATGAAGCTGGACATTCCTCTCTGGCCCAATGGCCCTCCTCTCTGCTGCTATGAC 60

QY 61 tctgtccctcgtgtcctccagtggaacctgtgcaccttctgtggtcgtgtgagga 120

Db 61 TCTGTCTCTGACACCTCCAGTGGGACCTGCTTTGTGGCTGTGTGAGGAA 120

QY 121 ttacttctcctggccaagaagcagagctgcaaggagcctcggatcacacagatgctgc 180

Db 121 TTCACTTTCATGGCCCAAGAACCGCTGCAGGGGACTTGGGATCACACAGATGCTGC 180

QY 181 tggagctgctgtgagacctggag 204

Db 181 TGGGCGCTGCGAGACCTGGAG 204

RESULT 10

AST251658 1060 bp mRNA linear VRT 03-OCT-2000

LOCUS AST251658

DEFINITION Acipenser baeri mRNA for follicle-stimulating hormone (FSH gene).

ACCESSION AJ251658

VERSION AJ251658.1 GI:8250131

KEYWORDS follicle-stimulating hormone; FSH gene.

SOURCE Siberian sturgeon.

ORGANISM Acipenser baeri

REFERENCE 1 (bases 1 to 1060)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;

Acipenserinae; Acipenser.

Querat B., Sellouk A. and Salmon C.

Phylogenetic analysis of the vertebrate glycoprotein hormone family

including new sequences of sturgeon (Acipenser baeri) beta subunits

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2002, 21:20:08 ; Search time 238.01 Seconds
(without alignments)
2813.313 Million cell updates/sec

Title: US-09-723-970-2

Perfect score: 390

Sequence: 1 atgaagctgagcttcctc.....ccacgagtgagacacac 390

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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8: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
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19: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	100.0	390	22	AAH46586
2	390	100.0	390	24	AAH46586
3	390	100.0	390	22	AAH46586
4	390	100.0	390	22	AAH46586
5	378	96.9	390	22	AAH46586
6	378	96.9	390	22	AAH46586
7	300.4	77.0	390	24	AAH46586
8	290.8	74.6	390	22	AAH46586
9	260	66.7	390	22	AAH46586

10	252	64.6	1045	22	AAH42568
11	156	40.0	2985	24	AAH42568
12	61.6	15.8	496	7	AAH42568
13	57.8	14.8	525	21	AAH42568
14	56.8	14.6	535	22	AAH42568
15	56.8	14.6	5651	22	AAH42568
16	53	13.6	524	19	AAH42568
17	53	13.6	511	19	AAH42568
18	51.4	13.2	843	19	AAH42568
19	50.4	12.9	616	11	AAH42568
20	50.2	12.9	486	10	AAH42568
21	48.8	12.5	278	21	AAH42568
22	48.8	12.5	309	21	AAH42568
23	48.8	12.5	312	21	AAH42568
24	48.8	12.5	312	21	AAH42568
25	48.8	12.5	315	21	AAH42568
26	48.8	12.5	315	21	AAH42568
27	48.8	12.5	315	21	AAH42568
28	48.8	12.5	318	21	AAH42568
29	48.8	12.5	318	21	AAH42568
30	48.8	12.5	318	21	AAH42568
31	48.8	12.5	321	21	AAH42568
32	48.8	12.5	321	21	AAH42568
33	48.8	12.5	321	21	AAH42568
34	48.8	12.5	324	21	AAH42568
35	48.8	12.5	324	21	AAH42568
36	48.8	12.5	324	21	AAH42568
37	48.8	12.5	327	21	AAH42568
38	48.8	12.5	327	21	AAH42568
39	48.8	12.5	327	21	AAH42568
40	48.8	12.5	330	21	AAH42568
41	48.8	12.5	330	21	AAH42568
42	48.8	12.5	333	21	AAH42568
43	48.8	12.5	333	21	AAH42568
44	48.8	12.5	348	18	AAH42568
45	48.8	12.5	348	18	AAH42568

ALIGNMENTS

RESULT 1	
AAH46586	AAH46586 standard; DNA: 390 BP.
XX	XX
AC	AAH46586;
XX	XX
DT	17-SEP-2001 (first entry)
XX	XX
DE	Human anterior pituitary hormone-related polynucleotide #1.
XX	XX
KW	Human; anterior pituitary hormone; hypertension; autoimmune disease;
KW	heart failure; ds.
XX	XX
OS	Homo sapiens.
PN	W0200144475-A1.
XX	XX
PD	21-JUN-2001.
XX	XX
PF	15-DEC-2000; 2000MO-JP08896.
XX	XX
PR	17-DEC-1999; 99JP-0358707.
PR	18-FEB-2000; 2000JP-0046825.
XX	XX
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	XX
PI	Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX	XX
DR	WPI: 2001-408485/43.
DR	P-PDB; AAG64064.
XX	XX
PT	Polypeptides for treatment of hypertension, autoimmune disease and

```
PT heart failure -
XX
XX Claim 7, Fig 1; 107pp; Japanese.
XX
CC The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence encodes
CC the polypeptide of the invention.
XX
XX Sequence 390 BP; 69 A; 128 C; 106 G; 87 T; 0 other:

Query Match          100.0%; Score 390; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 4.7e-102;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaagctggcattctctctctctggcccatggccctcctctctgtgctatggc 60
    |||
DB 1 atgaagctggcattctctctctctggcccatggccctcctctctgtgctatggc 60
    |||

QY 61 tgtgtcctcggtgctccagctgggaacctggcaaccttgggtggtcgtgcaaggag 120
    |||
DB 61 tgtgtcctcggtgctccagctgggaacctggcaaccttgggtggtcgtgcaaggag 120
    |||

QY 121 ttacttctctggccaagaagcagctgcaaggccttcgataccaacagatgcctgc 180
    |||
DB 121 ttacttctctggccaagaagcagctgcaaggccttcgataccaacagatgcctgc 180
    |||

QY 181 tgggtgcgtgtgagacctgggaaccattctggaacccctatatattgaagccat 240
    |||
DB 181 tgggtgcgtgtgagacctgggaaccattctggaacccctatatattgaagccat 240
    |||

QY 241 catcagctcgtacctacaacagcaagcaagctgacttcaagctggcccaactgtgc 300
    |||
DB 241 catcagctcgtacctacaacagcaagcaagctgacttcaagctggcccaactgtgc 300
    |||

QY 301 ccggagctcgaccctctctacactatccgtggccatccgctgtgactcggaagctgc 360
    |||
DB 301 ccggagctcgaccctctctacactatccgtggccatccgctgtgactcggaagctgc 360
    |||

QY 361 tccactgcccacacagagatgtgagaccatc 390
    |||
DB 361 tccactgcccacacagagatgtgagaccatc 390
    |||

RESULT 2
AAS17500
ID AAS17500 standard; cDNA; 390 BP.
XX
XX AAS17500;
XX
XX 14-FEB-2002 (first entry)
XX
XX DNA encoding human beta-like glycoprotein hormone, Beta10.
XX
XX Human; glycoprotein hormone; beta10; homeostatic disorder; diabetes;
XX stress response; immune system dysfunction; tissue damage; cancer;
XX thyroid gland related condition; ss.
XX
XX Homo sapiens.
XX
XX Key sig_peptide Location/Qualifiers
XX sig_peptide 1..72
XX CDS 1..390
XX /tag- a
XX /tag- b
XX /product- "beta-like glycoprotein beta10"
XX /partial
XX /note- "No stop codon given"
```

```
FT mat_peptide 73..390
FT /tag- c
FT /note- "Mature beta10"
XX
XX WO200173034-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09999.
XX
XX 28-MAR-2000; 2000US-192654P.
XX 24-APR-2000; 2000US-199211P.
XX 27-NOV-2000; 2000US-0723970.
XX
XX (AMGE-) AMGEN INC.
XX
XX Paszty CJR, Cao J, Danilenko DM, Gong J, Hill DC;
XX WPI; 2002-055150/07.
XX P-PSDB: AAU10366.
XX
XX New polynucleotides encoding polypeptides for treating and diagnosing
XX disorders such as thyroid gland related conditions comprises novel
XX human glycoprotein hormone polypeptide, and the beta10 protein -
XX
XX Claim 1, Fig 1; 201pp; English.
XX
XX The invention relates to an isolated polynucleotide (1) encoding
XX beta-like glycoprotein polypeptide. The polynucleotides, polypeptides and
XX heterodimers can be administered therapeutically (e.g. by administering
XX the polynucleotides to modulate levels of beta10 polypeptide or
XX heterodimer; to treat or prevent diseases and disorders such as
XX homeostatic disorders (e.g. diabetes), disorders related to stress
XX responses (e.g. immune system dysfunction) or disorders requiring
XX increased cell differentiation/proliferation (e.g. tissue damage during
XX cancer treatment). They can be included in compositions which are used
XX for the same purposes. They are useful to diagnose pathological
XX conditions or susceptibility to pathological conditions, especially
XX thyroid gland related conditions. The polypeptides and heterodimers can
XX be used to identify binding compounds. They are useful for producing
XX antibodies, and for detecting or quantifying beta10 polypeptides,
XX heterodimers, and selective binding agents. The polynucleotides can be
XX used to produce cells comprising the polynucleotide, and for producing
XX polypeptides/heterodimers and identifying compounds modulating beta 10
XX polypeptide/heterodimer activity by detecting changes in activity or
XX production in the cell. They can also be used to produce implantation
XX devices to administer polypeptide/heterodimers. The present
XX sequence represents the DNA encoding beta-like glycoprotein hormone
XX beta10.
XX
XX Sequence 390 BP; 69 A; 128 C; 106 G; 87 T; 0 other:

Query Match          100.0%; Score 390; DB 24; Length 390;
Best Local Similarity 100.0%; Pred. No. 4.7e-102;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
DB 1 atgaagctggcattctctctctctggcccatggccctcctctctgtgctatggc 60
    |||

QY 61 tgtgtcctcggtgctccagctgggaacctggcaaccttgggtggtcgtgcaaggag 120
    |||
DB 61 tgtgtcctcggtgctccagctgggaacctggcaaccttgggtggtcgtgcaaggag 120
    |||

QY 121 ttacttctctggccaagaagcagctgcaaggccttcgataccaacagatgcctgc 180
    |||
DB 121 ttacttctctggccaagaagcagctgcaaggccttcgataccaacagatgcctgc 180
    |||

QY 181 tgggtgcgtgtgagacctgggaaccattctggaacccctatatattgaagccat 240
    |||
DB 181 tgggtgcgtgtgagacctgggaaccattctggaacccctatatattgaagccat 240
    |||
```

QY 241 catgagctctgtacctcaacagagacaaacaggtgactgtcaagctgtgcccactgtgccc 300
 Db 241 catgagctctgtacctcaacagagacaaacaggtgactgtcaagctgtgcccactgtgccc 300
 QY 301 ccggagagtcgagccctctctacactatcccggtgacatccgctgtgactgtgagagccctgc 360
 Db 301 ccggagagtcgagccctctctacactatcccggtgacatccgctgtgactgtgagagccctgc 360
 QY 361 tccactgcccacacgagagtgtagacatc 390
 Db 361 tccactgcccacacgagagtgtagacatc 390
 RESULT 3
 AAD16347
 ID AAD16347 standard; DNA; 393 BP.
 AC AAD16347;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human sbhGTA gene.
 XX
 KW Human: Alzheimer's disease; amyotrophic lateral sclerosis;
 KW ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia;
 KW inflammation; haematopoietic disease; anxiety; feeding disorder; aging;
 KW anorexia; depression; cardiovascular disease; sleep disorder; seizure;
 KW memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia;
 KW sexual disorder; growth abnormality; infection; autoimmune disease;
 KW rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis;
 KW cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease;
 KW hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity;
 KW diabetes mellitus; glomerulonephritis; renovascular hypertension;
 KW cancer; vaccine; gene therapy; sbhGTA gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..393
 FT /tag= a
 FT /product= "Human sbhGTA protein"
 XX
 PN W0200160850-A1.
 XX
 PD 23-AUG-2001.
 PD
 PF 14-FEB-2001; 2001MO-US04703.
 PF
 XX 14-FEB-2000; 2000US-0182172.
 PR 29-FEB-2000; 2000US-0186084.
 PR 18-APR-2000; 2000US-0198583.
 PR 04-OCT-2000; 2000US-0237963.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 XX
 DR WPI: 2001-536566/59.
 DR P-PDB: AA09440.
 XX
 PT New secreted and membrane associated polypeptides for treating
 PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
 PT disorders, stroke, and asthma
 XX
 PS Claim 2; Page 38; 94pp: English.
 XX
 CC The present sequence is a gene encoding human sbhGTA protein,
 CC a secreted protein of the invention.
 CC The invention relates to secreted and membrane associated polypeptides
 CC and nucleic acid molecules encoding such polypeptides. Sequences of the
 CC invention are useful for treating diseases such as Alzheimer's disease,
 CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases

CC of the immune system, haematopoietic disease, inflammation, anxiety,
 CC schizophrenia, feeding disorders, anorexia, depression, social, sexual
 CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning
 CC and memory alteration and altered immune response, seizure, migraine,
 CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
 CC of transsexuals, growth abnormalities, obesity, infections, autoimmune
 CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
 CC disorders associated with healthy maintenance of gastric mucosa and
 CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
 CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
 CC amnesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
 CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
 CC viral and non-viral hepatitis, type I and type II diabetes mellitus,
 CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
 CC paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
 CC invention are used to identify membrane bound and soluble receptors.
 CC They are also useful as vaccines for inducing an immunological response
 CC in a mammal. Polynucleotides of the invention are used in gene therapy.
 CC They are also valuable for chromosome localisation studies and tissue
 CC expression studies.
 XX
 SO Sequence 393 BP; 70 A; 128 C; 107 G; 88 T; 0 other;
 XX
 Query Match 100.0%; Score 390; DB 22; Length 393;
 Best Local Similarity 100.0%; Pred. No. 4,7e-102;
 Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 atgaagctcgagatctctctctctctgcccacatgagccctctctctgtgctgtatgac 60
 Db 1 atgaagctcgagatctctctctctctctgcccacatgagccctctctgtgctgtatgac 60
 QY 61 tgtgcccggctgcccctcagtcgagacctgagccactgtgggtgtggtgcgtgagggag 120
 Db 61 tgtgcccggctgcccctcagtcgagacctgagccactgtgggtgtggtgcgtgagggag 120
 QY 121 ttactctctgcccagaagacagagctgacagggcctctgagatcacacagatgctgcg 180
 Db 121 ttactctctgcccagaagacagagctgacagggcctctgagatcacacagatgctgcg 180
 QY 181 tggggtcgctgtgagactgtgagaaacacatctcgaaacccctatatggaagccat 240
 Db 181 tggggtcgctgtgagactgtgagaaacacatctcgaaacccctatatggaagccat 240
 QY 241 catcagagctgtacctaacagagacaaacaggtgactgtcaagctgtccaaactgtgccc 300
 Db 241 catcagagctgtacctaacagagacaaacaggtgactgtcaagctgtccaaactgtgccc 300
 QY 301 ccggagagtcgagccctctctacactatcccggtgacatccgctgtgactgtgagagccctgc 360
 Db 301 ccggagagtcgagccctctctacactatcccggtgacatccgctgtgactgtgagagccctgc 360
 QY 361 tccactgcccacacgagagtgtagacatc 390
 Db 361 tccactgcccacacgagagtgtagacatc 390
 RESULT 4
 AAH42567
 ID AAH42567 standard; DNA; 917 BP.
 AC AAH42567;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Nucleotide sequence of a human cystine knot polypeptide.
 XX
 KW Cysteine knot polypeptide; follicular arrest; recruitment modulator;
 KW fertility-related disorder; contraception; menopause; contraceptive;
 KW follicle growth, ss.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
CDS 101..493
/*tag= a
/product= "cystine knot polypeptide"

MO200153346-A1.

26-JUL-2001.

17-JAN-2001; 2001WO-EP00570.

18-JAN-2000; 2000EP-0200185.

(ALKU) AKZO NOBEL NV.

Moselman S, Spek Van Der Pj;

WPI: 2001-476102/51.

P-PSDB: AAG63211.

New DNA sequences, useful for coding or producing cystine knot polypeptides, which are useful in preparing a pharmaceutical for fertility-related disorders or contraception, and for controlling follicular arrest and recruitment.

Claim 6; Page 23; 29pp; English.

The present sequence encodes a human cystine knot polypeptide. The polypeptide is a follicular arrest and recruitment modulator. Cystine knot polypeptides are useful in preparing a pharmaceutical for fertility-related disorders or in contraception. The polypeptide is particularly useful for controlling follicular arrest and recruitment. Inhibition of recruitment can be used to delay (premature) menopause or as a contraceptive. The polypeptide is also useful for in vitro maturation and growth of follicles, e.g. from frozen ovarian tissue.

Sequence 917 BP; 222 A; 249 C; 205 G; 241 T; 0 other:

Query Match 100.0%; Score 390; DB 22; Length 917;
Best Local Similarity 100.0%; Pred. No. 6.1e-102; Mismatches 0; Indels 0; Gaps 0;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaagctgacattcctctctctgcccacatgacctctctctctctgctgctatgac 60
|||||
DB 101 atgaagctgacattcctctctctctgcccacatgacctctctctctgctgctatgac 160
|||||

QY 61 tgtgtccctgctgctcctcagtgaggacctgttggtggtctgctgctgaggag 120
|||||
DB 161 tgtgtccctgctgctcctcagtgaggacctgttggtggtctgctgctgaggag 220
|||||

QY 121 tttaattcttcgccaagaagaagctgcaaggccttcctctctctctctgctgctatgac 180
|||||
DB 221 tttaattcttcgccaagaagaagctgcaaggccttcctctctctctctgctgctatgac 280
|||||

QY 181 tggggctgctgtgagacctgaggagaaccattctggaacccctctatattgaagccat 240
|||||
DB 281 tggggctgctgtgagacctgaggagaaccattctggaacccctctatattgaagccat 340
|||||

QY 241 catcagagctgtaactacaacagacaaacagtgactgtcaagctbcccacactgtgcc 300
|||||
DB 341 catcagagctgtaactacaacagacaaacagtgactgtcaagctbcccacactgtgcc 400
|||||

QY 301 ccgggagtcgaaccctctacaacatccgtgtgacatccgtgtgactgagagctgtgc 360
|||||
DB 401 ccgggagtcgaaccctctacaacatccgtgtgacatccgtgtgactgagagctgtgc 460
|||||

QY 361 tccactgcacacagagagtgtagacatc 390
|||||
DB 461 tccactgcacacagagagtgtagacatc 490
|||||

RESULT 5

AAFB8367
ID AAFB8367 standard; cDNA: 693 BP.
XX
AC AAFB8367;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human novel gonadotropin (NOVGON) protein encoding cDNA.
XX
KW NOVG: transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
antibacterial; cerebroprotective; antidiabetic; antiarthritic;
antiallergic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..693
CDS /*tag= a
/product= "NOVGON"

MO200140291-A2.

07-JUN-2001.

06-DEC-2000; 2000WO-US33029.

06-DEC-1999; 99US-0169056.
09-DEC-1999; 99US-0169866.
09-DEC-1999; 99US-0169886.
10-DEC-1999; 99US-0170252.
12-JAN-2000; 2000US-0175740.
05-DEC-2000; 2000US-0170252.

(CURA-) CURAGEN CORP.

Burgess CE, Prayaga SK, Shinkels RA, Rastelli L, Zernhusen BD;
Mezes PS;
WPI: 2001-374790/39.
P-PSDB: AAB84998.

Novel isolated human transmembrane, neuromedin peptide
gonadotropin-like protein and interleukin-1 receptor antagonist
proteins, useful for treating cancer, immune response disorder,
metabolic function disorders

Claim 8; Fig 6A; 138pp; English.

The invention provides novel polypeptides (NOV) selected from human
transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
antagonist proteins (NOVINTRA A and B). The invention also provides
methods in which a NOV polypeptide, polynucleotide and antibody are
used in the detection, prevention and treatment of a broad range of
pathological states. NOVTRAN can be used to treat is a cell signaling
disorder such as cancer, immune response disorder, hematopoietic
disorder, neurodegenerative disorder. NOVNEUR can be used to treat
endocrine disorder, muscle disorder, neurologic disorder, cancers of
central nervous system, breast, colon, ovary, kidney, prostate and
thyroid. NOVGON can be used to treat reproductive development disorder,
metabolic function disorder and melanoma. NOVINTRA A and B can be used
to treat bone metabolism or structure disorder, inflammatory response
disorder, immune regulation disorder, septic shock, stroke, diabetes,
arthritis and cancer. The present sequence represents a cDNA encoding
the NOVGON polypeptide.

Sequence 693 BP; 138 A; 197 C; 196 G; 162 T; 0 other;

Query Match 96.9%; Score 378; DB 22; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;


```

PI Paszty GR, Cao J, Danilenko DM, Gong J, Hall DC;
XX
XX WPI: 2002-055150/07.
DR
DR P-PSDB; AAU010368.
XX
XX New polynucleotides encoding polypeptides for treating and diagnosing
PT disorders such as thyroid gland related conditions comprises novel
PT human glycoprotein hormone polypeptide, and the beta10 protein -
XX
PS Example 5; Page 194; 201pp; English.
XX
XX The invention relates to an isolated polynucleotide (1) encoding
CC beta-like glycoprotein polypeptide. The polynucleotides, polypeptides and
CC heterodimers can be administered therapeutically (e.g. by administering
CC the polynucleotides to modulate levels of beta10 polypeptide or
CC heterodimer; to treat or prevent diseases and disorders such as
CC homeostatic disorders (e.g. diabetes), disorders related to stress
CC responses (e.g. immune system dysfunction) or disorders requiring
CC increased cell differentiation/proliferation (e.g. tissue damage during
CC cancer treatment). They can be included in compositions which are used
CC for the same purposes. They are useful to diagnose pathological
CC conditions or susceptibility to pathological conditions, especially
CC thyroid gland related conditions. The polypeptides and heterodimers can
CC be used to identify binding compounds. They are useful for producing
CC antibodies, and for detecting or quantifying beta10 polypeptides,
CC heterodimers, and selective binding agents. The polynucleotides can be
CC used to produce cells comprising the polynucleotide, and for producing
CC polypeptides/heterodimers and identifying compounds modulating beta 10
CC polypeptide/heterodimer activity by detecting changes in activity or
CC production in the cell. They can also be used to produce implantation
CC devices to administer polypeptide/heterodimers. The present
CC sequence represents the DNA encoding mouse beta-like glycoprotein hormone
CC beta10.
XX
XX Sequence 393 BP; 78 A; 111 C; 109 G; 95 T; 0 other;
SQ
Query Match 77.0%; Score 300.4; DB 24; Length 393;
Best Local Similarity 85.6%; Pred. No. 2.1e-76;
Matches 334; Conservative 0; Mismatches 56; Indels 0; Gaps 0
QY 1 atgaagctggaattcctctccttctgcccacagagccctcctctctgtgctatgac 60
Db 1 atgaagttgtataactcttgcttgtagtgagccctcctcctctgtggtcctgac 60
QY 61 tgtgtccctcgtgtcctccagttggaacctgtgcaccttgttggtgtgtccgttgaggag 120
Db 61 tctgtccctcagagctccagttggaacctgtgcaccttgttggtgtgtccgttgaggag 120
QY 121 ttattcttcctgccaagaagccagaagctgccaaggggcttcggaataccacagagatgctgc 180
Db 121 ttcaatttcataggccaagaagccagagctgccaaggggcttcggaataccacagagatgctgc 180
QY 181 tggggtcgtgtgagacactgaggagaaccacattctggaacccccctataattgaagccat 240
Db 181 tggggccgctgagagacactgaggagaaccacattctggaacccccctataattgaagccat 240
QY 241 catcagatctgtaacttaacaagagacaacaggtgtacgttcaagctgcccaactgtgcc 300
Db 241 catcagatgtgtatacaataagagacaacaggtgtacagttgaagctgctctaactgtgcc 300
QY 301 ccgggagatgcagccctttacaacatacccggtggccatccgcgtgtacatgcagagcctgc 360
Db 301 cctggagatgcagccctttacaacatacccggtggccatccgcgtgtacatgcagagcctgc 360
QY 361 tccactgcccacacagagatgtgagaccalc 390
Db 361 tccactgcccacacatgagtgtgagaccalc 390
RESULT 8
ID AAH46593
AAH46593 standard; DNA; 387 BP.

```

XX	AHA46593:
AC	
XX	
DT	17-SEP-2001 (first entry)
XX	
DE	Rat anterior pituitary hormone-related polynucleotide #1.
XX	
KW	Rat; anterior pituitary hormone; hypertension; autoimmune disease;
KW	heart failure; ds.
OS	
XS	Rattus sp.
XX	
PN	M0200144475-A1.
XX	
PD	21-JUN-2001.
XX	
PF	15-DEC-2000; 2000MO-JP08896.
FP	
PR	17-DEC-1999; 99JP-0358707.
PR	18-FEB-2000; 2000JP-0046825.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX	
DR	WPI: 2001-408485/43.
DR	P-PSDB: AAG64067.
XX	
PT	Polypeptides for treatment of hypertension, autoimmune disease and heart failure -
XX	
PS	Claim 7: Page 103; 107pp; Japanese.
XX	
CC	The invention relates to a novel polypeptide comprising a fully defined
CC	130 amino acid sequence given in the specification and its amides,
CC	esters and salts. The polypeptide has anterior pituitary hormone-related
CC	activity. It is useful for the treatment of hypertension, autoimmune
CC	diseases and heart failure. The screening method and kit also
CC	provided in the invention are useful for identifying new substances
CC	for treating and preventing these diseases. The present sequence is
CC	is a polynucleotide encoding a polypeptide provided in the specification.
XX	
SQ	Sequence 387 BP; 77 A; 110 C; 108 G; 92 T; 0 other;

Query Match 74.6%; Score 290.8; DB 22; Length 387;
 Best Local Similarity 85.9%; Pred. No. 1.2e-73;
 Matches 335; Conservative 0; Mismatches 52; Indels 3; Gaps 1.

QY	1	atgaagcgggatacttcttccttgccgcccatgagccctctctctctgtgcctatgac	60
Db	1	atgaagcgcygataactctgtcctgtgtaactcgagc---ctctctctgggtgctctgac	57
QY	61	tgtgtccctcgytgcctccagltgagaacctgcgcaacttgtttgggtcgtgcgtgaaggag	120
Db	58	tctgtcccacagagctccagcgsggaacctaccacacttttgtggatgtgcttggggaa	117
QY	121	ttacttcctcgtgcacaagaagcaggtcgtcagggtgaccttcggaaccaacagatgcttcg	180
Db	118	ttcaccttttgtgcacaagaagcaggtcgtcagggtgaccttcggaaccaacagatgcttcg	177
QY	181	tgggtgtcgtgtggaagacctgggagaaaccaatcttcggaaacccccctatatgaaagccat	240
Db	178	tgggtgtcgtgtggaagacctgggagaagaacccaatcttcggagcctccccaataaagccat	237
QY	241	catacgaagtgtacctatacaacagagaccaaacaggtgtacgtltaagctgcgcaactgtgc	300
Db	238	catacgaagtgtacctatacaatgagaccagaaggtgtgaagcgtgctaactgtgc	297
QY	301	cctggagatgcagacccttctatacaactatcccgtyggccatcgcgtgtgactcgtgaagcttcg	360
Db	298	cctggagatgcagacccttctatacaactatacgtgtcttcgaatgtactcgtcggggatgt	357

QY 361 tcaactgcacacagagtgtagaccatc 390
|||||
Db 358 tccactgcccacactgagtgtagaccatc 387

RESULT 9

AAH46594
ID AAH46594 standard; DNA; 318 BP.

AAH46594;

17-SEP-2001 (first entry)

Rat anterior pituitary hormone-related polynucleotide #2.

Rat; anterior pituitary hormone; hypertension; autoimmune disease;

heart failure; ds.

Rattus sp.

WO200144475-A1.

21-JUN-2001.

15-DEC-2000; 2000WO-JP08896.

17-DEC-1999; 99JP-0358707.

18-FEB-2000; 2000JP-0046825.

(TAKE) TAKEDA CHEM IND LTD.

Hinuma S, Fukusumi S, Fujii R, Hosoya M;

WPI; 2001-408485/43.

P-PSDB; AAG64068.

Polypeptides for treatment of hypertension, autoimmune disease and

heart failure -

Claim 7; Page 104; 107pp; Japanese.

The invention relates to a novel polypeptide comprising a fully defined

130 amino acid sequence given in the specification and its amides,

esters and salts. The polypeptide has anterior pituitary hormone-related

activity. It is useful for the treatment of hypertension, autoimmune

diseases and heart failure. The screening method and kit also

provided in the invention are useful for identifying new substances

for treating and preventing these diseases. The present sequence is

is a polynucleotide encoding a polypeptide provided in the specification.

Sequence 318 BP; 69 A; 89 C; 90 G; 70 T; 0 other;

Query Match 66.7%; Score 260; DB 22; Length 318;

Best Local Similarity 88.9%; Pred. No. 7.2e-65;

Matches 281; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 315 ctctacactatccgtgaccatccgtctgtagtcgcgcagcgtctcactgcaccac 374
|||||
Db 243 ctctacactacactacactgctgcgatgtgactgaggcagatgttccactgcccacc 302

RESULT 10

AAH42568
ID AAH42568 standard; DNA; 1045 BP.

AAH42568;

01-OCT-2001 (first entry)

Nucleotide sequence of human cystine knot polypeptide splice variant.

Cystine knot polypeptide; follicular arrest; recruitment modulator;

fertility-related disorder; contraception; menopause; contraceptive;

follicle growth; ss.

Homo sapiens.

WO200153346-A1.

26-JUL-2001.

17-JAN-2001; 2001MO-EP00570.

18-JAN-2000; 2000EP-0200185.

(ALKU) AKZO NOBEL NV.

Mosselman S, Spek Van Der PJ;

WPI; 2001-476102/51.

P-PSDB; AAG63212.

New DNA sequences, useful for coding or producing cystine knot

polypeptides, which are useful in preparing a pharmaceutical for

follicular arrest and recruitment -

Claim 7; Page 24; 29pp; English.

The present sequence encodes a human cystine knot polypeptide splice

variant. The polypeptide is a follicular arrest and recruitment

modulator. Cystine knot polypeptides are useful in preparing a

pharmaceutical for fertility-related disorders or in contraception.

The polypeptide is particularly useful for controlling follicular

arrest and recruitment. Inhibition of recruitment can be used to delay

(premature) menopause or as a contraceptive. The polypeptide is also

useful for in vitro maturation and growth of follicles, e.g. from

frozen ovarian tissue.

Sequence 1045 BP; 254 A; 279 C; 234 G; 278 T; 0 other;

Query Match 64.6%; Score 252; DB 22; Length 1045;

Best Local Similarity 75.3%; Pred. No. 2e-62;

Matches 390; Conservative 0; Mismatches 128; Gaps 1;

QY 1 atgaagctgcatctcctctctgagccatgaccctcctctctgctgctatgac 60
|||||
Db 101 atgaagctgcatctcctctctgagccatgaccctcctcctctctgctgctatgac 160

QY 61 tttgtctctggtgctcccaagtggaacccgacaccttctgtggtctgtccgtgagag 120
|||
Db 161 tctgtctctggtgctcccaagtggaacccgacaccttctgtggtctgtccgtgagag 220
QY 121 tttacttctctggaagaagcagagctgcaagggtcttcgagtcacacacagatgctgc 180
Db 221 tttacttctctggaagaagcagagctgcaagggtcttcgagtcacacacagatgctgc 280
QY 181 tgggtgctgctgtgagacacgtggag----- 204
|||
Db 281 tgggtgctgctgtgagacacgtggagctttgtcaagatgctgtatgaacaagcatca 340
QY 205 ----- 204
Db 341 atacacattgttgtgtgacgtgagatgagacctccctgagctgtagatccctcagcct 400
QY 205 -----aaaccattctgtgaaccccccataatg 232
|||
Db 401 aatggaagggcatttagaatcacactgtgacataaccacattcggaaaccccccataatg 460
QY 233 aagcccatcatcgagctctgtacatacaagagacaaagaagtgtacgttcaagctgccca 292
|||
Db 461 aagcccatcatcgagctctgtacatacaagagacaaagaagtgtacgttcaagctgccca 520
QY 293 acgtgtgccccggagatcgagaccctctacacactatccggtggcaccgtgtgactgcg 352
|||
Db 521 acgtgtgccccggagatcgagaccctctacacactatccggtggcaccgtgtgactgcg 580
QY 353 gagcctgtccactgcgacacacagaggtgtgagacatc 390
|||
Db 581 gagcctgtccactgcgacacacagaggtgtgagacatc 618

RESULT 11
ID AAS17518 standard; DNA; 2985 BP.
XX AAS17518;
AC AAS17518;
XX 14-FEB-2002 (first entry)
XX
XX Genomic DNA encoding mouse beta-1-like glycoprotein hormone, beta10.
DE
XX
XX Mouse; glycoprotein hormone; beta10; homeostatic disorder: diabetes;
KM stress response; immune system dysfunction; tissue damage; cancer;
KW thyroid gland related condition; ds.
XX
XX Mus musculus.
OS
XX
XX WO200173034-A2.
PN
XX
XX 04-OCT-2001.
PD
XX
XX 28-MAR-2001; 2001WO-US09999.
PF
XX
XX 28-MAR-2000; 2000US-192654P.
PR 24-APR-2000; 2000US-199211P.
PR 27-NOV-2000; 2000US-0723970.
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Paszty CJR, Cao J, Danilenko DM, Gong J, Hill DC;
PI
XX
XX WPI; 2002-055150/07.
DR
XX
XX New polynucleotides encoding polypeptides for treating and diagnosing
PT disorders such as thyroid gland related conditions comprises novel
PT human glycoprotein hormone polypeptide, and the beta10 protein -
XX
XX Example 6; Page 198-199; 201pp; English.
XX
XX The invention relates to an isolated polynucleotide (I) encoding
CC beta-1-like glycoprotein polypeptide. The polynucleotides, polypeptides and

CC heterodimers can be administered therapeutically (e.g. by administering
CC the polynucleotides to modulate levels of beta10 polypeptide or
CC heterodimer; to treat or prevent diseases and disorders such as
CC homeostatic disorders (e.g. diabetes), disorders related to stress
CC responses (e.g. immune system dysfunction) or disorders requiring
CC increased cell differentiation/proliferation (e.g. tissue damage during
CC cancer treatment). They can be included in compositions which are used
CC for the same purposes. They are useful to diagnose pathological
CC conditions or susceptibility to pathological conditions, especially
CC thyroid gland related conditions. The polypeptides and heterodimers can
CC be used to identify binding compounds. They are useful for producing
CC antibodies, and for detecting or quantifying beta10 polypeptides,
CC heterodimers, and selective binding agents. The polynucleotides can be
CC used to produce cells comprising the polynucleotide, and for producing
CC polypeptides/heterodimers and identifying compounds modulating beta 10
CC polypeptide/heterodimer activity by detecting changes in activity or
CC production in the cell. They can also be used to produce implantation
CC devices to administer polypeptide/heterodimers. The present sequence
CC represents the genomic DNA encoding mouse beta-1-like glycoprotein hormone
CC beta10.
XX
SQ Sequence 2985 BP; 784 A; 630 C; 761 G; 810 T; 0 other;
XX

Query Match 40.0%; Score 156; DB 24; Length 2985;
Best Local Similarity 85.3%; Pred. No. 8, 4e-35;
Matches 174; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 atgaagctgacattctctctcttctgcccacatggccctctctctgtgctgactgc 60
|||
Db 1 atgaagttgtataacttctctctgtgctgagtgccctctctctctgtggtgacctgcac 60
QY 61 tttgtctcgtgtgctcctcagatgggaacctgagcacttgttggtctgtgcgtgagagag 120
|||
Db 61 tctgtcctcagacgctccagctggaacctgcacacttgttggtctgtgtgagagag 120
QY 121 tttacttctctggaagaagcagagctgcaagggtcttcgatacacacagatgctgc 180
|||
Db 121 tttacttctatggccaagaagcagagctgcaagggtcttcgatacacacagatgctgc 180
QY 181 tgggtgctgctgtgagacacctggag 204
|||
Db 181 tgggtgctgctgtgagacacctggag 204

RESULT 12
ID AAN60523 standard; cDNA; 496 BP.
XX AAN60523;
AC AAN60523;
XX
XX 01-JUL-1991 (first entry)
DT
XX
XX Sequence encoding dog beta luteinising hormone (LH).
DE
XX
XX Contraceptive; fertility control; vaccine; reproductive hormone; ss.
KM
XX
XX Dog.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..54
FT mat_peptide 55..420
FT /*tag= a
FT /*tag= b
FT polyA_signal 457..462
FT /*tag= c
FT polyA_site 496
FT /*tag= d
XX
XX WO8607383-A.
PN
XX
XX 18-DEC-1986.
PD
XX
XX

PF 04-JUN-1986; 86WO-US01226.
XX
XX 18-JUL-1985; 85US-0756847.
PR 04-JUN-1985; 85US-0741168.
XX
XX (BIOT-) BIOTECHN RES PARTN.
XX
XX Talmadge KD, Fildes JC;
XX
XX WPI; 1986-346608/52.
DR P-PSDB; AAP60601.
XX
XX Auto-antigen vaccines conferring antigenicity using multimers
PT etc. - useful as species specific or cross-species effective,
PS esp. for controlling fertility in mammals
XX
XX Example; Fig 3B; 101pp; English.
XX
XX The patentors claim a vaccine effective against mammalian fertility
CC comprising a vaccinia virus genome having disposed unit, in a non-
CC essential region, a DNA sequence of formula : (Hormone)_n; n=1-20;
CC Hormone= DNA sequence derived from the sequence encoding a
CC reproductive hormone. The hormone is esp. LH, GnRH, CG or FSH.
XX
XX Sequence 496 BP; 66 A; 191 C; 134 G; 105 T; 0 other;

Query Match 15.8%; Score 61.6; DB 7; Length 496;
Best Local Similarity 52.8%; Pred. No. 5.1e-08;
Matches 133; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 133 gccaaagacgagctgtagggccctcgatcaacagagatgctgtggtcgtgt 192
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 106 gctgagacgagcctgcgtctgtatcaacttcaacacacatctgtgcggtac 165
QY 193 gagacctgggaaacccatcttgaaacccctatatgtgaagccatcatcgatctgt 252
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 166 tgcacagcatgtagagtgctgcagcgcgcctgcacactgtgtcccaagcgaatgtgc 225
QY 253 acctacagagacacagtgactgtcaagctgcaactgtgcccggagatgcac 312
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 226 acctacacatgagctgacttgccttcaatccgctcccgatgtccgcctggcggtgac 285
QY 313 cccttctacactatcccgctggcactccgctgtgactgagagcctgtctcaactgcac 372
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 286 cccaatgctctctccctcccgctgacgctgtgcgtgtggcctgtctcaagcaac 345
QY 373 acgagagtgtgag 384
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 346 tccgactgtggg 357

RESULT 13
AAQ03844
ID AAQ03844 standard; cDNA; 525 BP.
XX
XX AAQ03844;
AC
XX
XX 24-AUG-1990 (first entry)
DT
XX
XX Bovine beta LH subunit.
DE
XX
XX Luteinizing hormone; follicle stimulating hormone;
KW recombinant cDNA; alpha subunit; beta subunit; ungulate; ss.
XX
XX Bos taurus.
OS
XX
XX
FH Key Location/Qualifiers
FT 3..422
FT CDS /*tag= a
FT /product=Bovine beta LH
XX
XX W09002757-A.

XX
XX 22-MAR-1990.
PD
XX
XX 02-SEP-1988; 88WO-0030949.
PE
XX
XX 02-SEP-1988; 88WO-US03049.
PR
XX
XX (INTE-) INTEGRATED GENETICS.
XX
XX Beck A, Bernstein E, Hsiung N, Kelton C, Lerner T, Reddy VB;
PI Chappel SC;
XX
XX WPI; 1990-115954/15.
DR
XX
XX Biologically active ungulate LH and FSH- produced by recombinant methods.
PT
XX
XX Disclosure; Fig 2; 66pp; English.
PS
XX
XX LH and FSH comprises an alpha and a beta subunit, both subunits can be
CC synthesised in a single cell conty. an expression vector comprising
CC heterologous DNA encoding one subunit.
CC See also AAQ03843-Q03851.
XX
XX Sequence 525 BP; 90 A; 202 C; 130 G; 103 T; 0 other;

Query Match 14.8%; Score 57.8; DB 11; Length 525;
Best Local Similarity 51.8%; Pred. No. 6.3e-07;
Matches 131; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 132 gccaaagacgagctgtagggccctcgatcaacagagatgctgtggtcgtgt 191
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 107 gctgagagagagcctgcgtctgtatcaacttcaacacagatctgcggtgta 166
QY 192 tgaacctgtggaaacccatcttgaaacccctatatgtgaagccatcatcgatctgt 251
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 167 ctgcacagcatgaaagcgggtgtcgtctgtatcattccgcacatgtcccaagcggtgtg 226
QY 252 tactacagagacacacagtgactgtcaagctgcaactgtgcccggagatgcga 311
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 227 caactacatgagctgctgccttcgctccgttcgctcccgctcccgatgtgagtgga 286
QY 312 cccttctacactatcccgctggcactccgctgtgactgagagcctgtctcaactgcac 371
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 287 cccaatgctctctccctcccgctgacgctgtgcgtgtggcctgtctcaagcaac 346
QY 372 cagagagtgtgag 384
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 347 cactgactgcggg 359

RESULT 14
AAH41044
ID AAH41044 standard; DNA; 535 BP.
XX
XX AAH41044;
AC
XX
XX 28-AUG-2001 (first entry)
DT
XX
XX GTH-beta LH subunit DNA.
DE
XX
XX Polymeric glycoprotein; goldfish; GTH; gonadotrophin; ds.
KW Carassius auratus.
OS
XX
XX JP2001086992-A.
PN
XX
XX
XX 03-APR-2001.
PD
XX
XX 24-SEP-1999; 99JP-0270790.
PE
XX
XX 24-SEP-1999; 99JP-0270790.
PR
XX
XX

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2002, 21:20:37 ; Search time 58.55 Seconds
(without alignments)
1636.158 Million cell updates/sec

Title: US-09-723-970-2

Perfect score: 390
Sequence: 1 atgaagctggcattcctctt.....ccacgagtgtagaccac 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1na/5a/COMB.seq.*
2: /cgn2_6/ptodata/2/1na/5b/COMB.seq.*
3: /cgn2_6/ptodata/2/1na/6a/COMB.seq.*
4: /cgn2_6/ptodata/2/1na/6b/COMB.seq.*
5: /cgn2_6/ptodata/2/1na/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/1na/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48.8	12.5	681	4	US-08-918-288-31
2	48.8	12.5	681	4	US-09-282-357-31
3	48.8	12.5	693	4	US-08-918-288-28
4	48.8	12.5	693	4	US-09-282-357-28
5	48.8	12.5	702	4	US-08-918-288-13
6	48.8	12.5	702	4	US-09-282-357-13
7	48.8	12.5	707	4	US-08-918-288-29
8	48.8	12.5	707	4	US-09-282-357-29
9	48.8	12.5	719	4	US-08-918-288-26
10	48.8	12.5	719	4	US-09-282-357-26
11	48.8	12.5	728	4	US-08-918-288-11
12	48.8	12.5	728	4	US-09-282-357-11
13	48.8	12.5	1006	1	US-08-239-256-1
14	46.4	11.9	718	4	US-08-918-288-10
15	46.4	11.9	718	4	US-09-282-357-10
16	46.4	11.9	744	4	US-08-918-288-8
17	46.4	11.9	744	4	US-09-282-357-8
18	45	11.5	726	4	US-08-918-288-16
19	45	11.5	726	4	US-09-282-357-16
20	45	11.5	752	4	US-08-918-288-14
21	45	11.5	752	4	US-09-282-357-14
22	43.2	11.1	549	4	US-08-918-288-37
23	43.2	11.1	549	4	US-09-282-357-37
24	43.2	11.1	575	4	US-08-918-288-35
25	43.2	11.1	575	4	US-09-282-357-35
26	43.2	11.1	717	4	US-08-918-288-7
27	43.2	11.1	717	4	US-09-282-357-7

28	43.2	11.1	743	4	US-08-918-288-5	Sequence 5, Appl1
29	43.2	11.1	743	4	US-09-282-357-5	Sequence 5, Appl1
30	43.2	11.1	834	4	US-08-918-288-4	Sequence 4, Appl1
31	43.2	11.1	834	4	US-09-282-357-4	Sequence 4, Appl1
32	43.2	11.1	835	4	US-08-918-288-40	Sequence 40, Appl1
33	43.2	11.1	835	4	US-09-282-357-40	Sequence 40, Appl1
34	43.2	11.1	836	4	US-08-918-288-2	Sequence 2, Appl1
35	43.2	11.1	836	4	US-09-282-357-2	Sequence 2, Appl1
36	43.2	11.1	837	4	US-08-918-288-38	Sequence 38, Appl1
37	43.2	11.1	837	4	US-09-282-357-38	Sequence 38, Appl1
38	43.2	11.1	893	4	US-09-142-320-3	Sequence 3, Appl1
39	43.2	11.1	893	4	US-09-142-320-5	Sequence 5, Appl1
40	43.2	11.1	893	4	US-09-142-320-6	Sequence 6, Appl1
41	43.2	11.1	893	4	US-09-142-320-7	Sequence 7, Appl1
42	43.2	11.1	893	4	US-09-142-320-8	Sequence 8, Appl1
43	43.2	11.1	893	4	US-09-142-320-9	Sequence 9, Appl1
44	43.2	11.1	893	4	US-09-142-320-10	Sequence 10, Appl1
45	43.2	11.1	1301	4	US-08-804-166-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-918-288-31/c
Sequence 31, Application US/08918288
Patent No. 6238890
GENERAL INFORMATION:
APPLICANT: BOIME, ILYING
APPLICANT: MOYLE, WILLIAM R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-918-288-31

	Query Match	12.5%	Score 48.8;	DB 4;	Length 681;
	Best Local Similarity	60.6%;	Pred. No. 3.8e-05;		
	Matches	80;	Conservative	0;	Mismatches 52; Indels 0; Gaps 0
Oy	250	tgtacctcaaacagagaccnaacaggatgactgtcacaagtgcgcccaactgtgtcccggaagtc	309		
Dd	471	TGTACTCTCAAGGAAGTGGATATATGAAACAGTAGAGAGTCCCGGGCTGTCTCACCATTGCA	412		
Oy	310	gaacccttcaaacctatactccgttgycgatccgctgtgactcgagagcctgtctccaaatgcc	369		
Dd	411	GATTTCCTTGTAATACATATACCACCACTGGCCACCCAGTGTCACTGTGGCGCAAGGTGCACACGCCAG	352		
Oy	370	accacggagatgt	381		
Dd	351	AGCACTGATTTGT	340		

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1 RESULT 2
2 US-09-282-357-31/c
3 : Sequence 31. Application US/09282357
4 Patent No. 6242580
5 : GENERAL INFORMATION:
6 APPLICANT: BOIME, Irving
7 APPLICANT: MOYLE, William R.
8 TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
9 TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
10 NUMBER OF SEQUENCES: 83
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: MORRISON & FOERSTER
13 STREET: 2000 Pennsylvania Avenue, NW, suite 5500
14 CITY: Washington
15 STATE: DC
16 COUNTRY: USA
17 ZIP: 20006-1888
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Diskette
20 COMPUTER: IBM Compatible
21 OPERATING SYSTEM: DOS
22 SOFTWARE: Fastseq for Windows Version 2.0
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/09/282,357
25 FILING DATE:
26 CLASSIFICATION: 536
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 08/918,288
29 FILING DATE: 25 AUG-1997
30 APPLICATION NUMBER: 08/853,524
31 FILING DATE: 09-MAY-1997
32 APPLICATION NUMBER: 08/199,382
33 FILING DATE: 18-FEB-1994
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Murashige, Kate H
36 REGISTRATION NUMBER: 29,959
37 REFERENCE/DOCKET NUMBER: 29500-20050.25
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 202-887-1500
40 TELEFAX: 202-887-0763
41 TELEX:
42 INFORMATION FOR SEQ ID NO: 31:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 681 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: double
47 TOPOLOGY: linear
48 US-09-282-357-31

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Query Match	12.5%	Score 48.8	DB 4	Length 681
Best Local Similarity	60.6%	Pred. No. 3.8e-05		
Matches	80	Conservative	0	Mismatches 52; Indels 0; Gaps 0
QY	250	tgtaactacaagagacaacacagcgtgcacagctgtcccaactgtgtcccccggagtc	309	

Db	471	TGTACCTTCAGAGAACTGGTATTATGAAAACATGTAGAGTGCGCCGGCTGTGCTGCACCAATGCA	412
Qy	310	gaccacctctacacactatcccgctggccatccgcgtctgacgtcgagagcgtctcactgccc	369
Dd	411	GATTCCCTTGTTATACATAACCCAGTGTGCCACCCAGTGTCTACTGTGTGGCAAGTGTGACAGCGAC	352
Qy	370	accacagagagtgat	381
Dd	351	AGCACTGATGTGT	340

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1      RESULT      3
2      US-08-918-288-28/c
3      : Sequence 28, Application US/08918288
4      : Patent No. 6238890
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: BOIME, Irving
8      : APPLICANT: MOYLE, William R.
9      : TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
10     : TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
11     : NUMBER OF SEQUENCES: 83
12     :
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: MORRISON & FOERSTER
15     : STREET: 2000 Pennsylvania Avenue, NW, suite 5500
16     : CITY: Washington
17     : STATE: DC
18     :
19     : COUNTRY: USA
20     : ZIP: 20006-1888
21     :
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: Diskette
24     : COMPUTER: IBM Compatible
25     : OPERATING SYSTEM: DOS
26     : SOFTWARE: FastSeq for Windows Version 2.0
27     :
28     : CURRENT APPLICATION DATA:
29     : APPLICATION NUMBER: US/08/918, 288
30     :
31     : FILING DATE:
32     : CLASSIFICATION:
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34     : PRIOR APPLICATION DATA:
35     : APPLICATION NUMBER: 09/282,357
36     :
37     : FILING DATE:
38     : APPLICATION NUMBER: 08/853,524
39     : FILING DATE: 09-MAY-1997
40     : APPLICATION NUMBER: 08/199,382
41     : FILING DATE: 18-FEB-1994
42     :
43     : ATTORNEY/AGENT INFORMATION:
44     : NAME: Murashige, Kate H
45     : REGISTRATION NUMBER: 29,959
46     : REFERENCE/DOCKET NUMBER: 29500-20050, 25
47     : TELECOMMUNICATION INFORMATION:
48     : TELEPHONE: 202-887-1500
49     : TELEFAX: 202-887-0763
50     :
51     : TELEX:
52     :
53     : INFORMATION FOR SEQ ID NO: 28:
54     :
55     : SEQUENCE CHARACTERISTICS:
56     : LENGTH: 693 base pairs
57     : TYPE: nucleic acid
58     : STRANDEDNESS: double
59     : TOPOLOGY: linear
60     :
61     :
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6
```

	Query Match	12.5%	Score 48.8	DB 4	Length 693
	Best Local Similarity	60.6%	Pred. No. 3.8e-05		
	Matches	80	Conservative	0	Indels 52
					Gaps 0
0y	250	ttlacttcaaacgagaccaaaccgtgacttgcacgtgcggccaactgtgcccggagtc	309		
Db	483	tctaccttcaaggaagactggtatataaacagtaagagtgccggctgtgcttaccatgca	424		
0y	310	gaccctcttaactatccgtggccatccgtgtgactgtggagagccgtcccaactgcc	369		
Db	423	gattctcttgatnaccatgccacccacgtgtcactgtggcagatgtagcagcagc	364		

OY 370 accacgagatgt 381
| | | | |
DB 363 AGCAGTGATTGT 352

RESULT 4

US-09-282-357-28/c
; Sequence 28, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 693 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-282-357-28

Query Match 12.5%; Score 48.8; DB 4; Length 693;
Best Local Similarity 60.6%; Pred. No. 3.8e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 250 tttacctaacaagagacaaacaggtgactgtcaagctgcccaactgtgccccggagtc 309
| | | | |
DB 483 tttaccttcaagaaactgtatgtgaaacagtagagctgcccgctgtctcacatgca 424
OY 310 gaccctctacaacctatcccgctggccatccgctgtgactgagagcctctccactgcc 369
| | | | |
DB 423 gattccttgaatgacatgacacagtgccacccagtgctgctgacgaagtgtgacagcgac 364
OY 370 accacgagatgt 381
| | | | |
DB 363 AGCAGTGATTGT 352

RESULT 5

US-08-918-288-13/c
; Sequence 13, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-918-288-13

Query Match 12.5%; Score 48.8; DB 4; Length 702;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

OY 250 tttacctaacaagagacaaacaggtgactgtcaagctgcccaactgtgccccggagtc 309
| | | | |
DB 492 tttaccttcaagaaactgtatgtgaaacagtagagctgcccgctgtctcacatgca 433
OY 310 gaccctctacaacctatcccgctggccatccgctgtgactgagagcctctccactgcc 369
| | | | |
DB 432 gattccttgaatgacatgacacagtgccacccagtgctgctgacgaagtgtgacagcgac 373
OY 370 accacgagatgt 381
| | | | |
DB 372 AGCAGTGATTGT 361

RESULT 6

US-09-282-357-13/c
; Sequence 13, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.

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; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Muraishige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-282-357-13

Query Match      12.5%; Score 48.8; DB 4; Length 702;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 ttactacaagagacaacacagtgactgtcaagctgccaactgtgccccggagatc 309
DB 492 ttactcttaaggaactggtatattgaaacagtgagagtcgccgctgtctcaccatgca 433
QY 310 gaccctcttacaactatccgltggccalcgcgtgtgactgcgagcctgtccactgcc 369
DB 432 gattctcttatatacattaccacagtgccaccagtcactgtggcamaagtgtacacggac 373
QY 370 accaaggagtg 381
DB 372 agcactgattgt 361

RESULT 7
US-09-918-288-29
; Sequence 29, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
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; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
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; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Muraishige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 707 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 33...698
; OTHER INFORMATION:
; US-09-918-288-29

Query Match      12.5%; Score 48.8; DB 4; Length 707;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 ttactacaagagacaacacagtgactgtcaagctgccaactgtgccccggagatc 309
DB 237 ttactcttaaggaactggtatattgaaacagtgagagtcgccgctgtctcaccatgca 296
QY 310 gaccctcttacaactatccgltggccalcgcgtgtgactgcgagcctgtccactgcc 369
DB 297 gattctcttatatacattaccacagtgccaccagtcactgtggcamaagtgtacacggac 356
QY 370 accaaggagtg 381
DB 357 agcactgattgt 368

RESULT 8
US-09-282-357-29
; Sequence 29, Application US/09282357
; Patent No. 6242360
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
```

```

? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/282,357
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/918,288
? FILING DATE: 25 AUG-1997
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 29:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 707 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 33...698
? OTHER INFORMATION:
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US-09-282-357-29

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Query Match          12.5%; Score 48.8; DB 4; Length 707;
Best Local Similarity 60.6%; Pred. No.3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tgaactacaagagacaaacaggtgactgcaagctgcccgaactgtgcccggagatc 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 237 tgaactctcaagaaactgataatgaacagtgagagctgccggcctgtgctacacatgca 296
QY 310 gaccctctcaacactatcccgtggccatccgcgtgtgactgagcgagctctccactgcc 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 297 gattccttgatatacattaccagtgccaccagtcactgtgtgcaagtgtgacagcgac 356
QY 370 accacgagatgt 381
    ||||| |||||
DB 357 agcactgattgt 368

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 26:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 719 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 33...700
? OTHER INFORMATION:
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US-08-918-288-26

```

```

Query Match          12.5%; Score 48.8; DB 4; Length 719;
Best Local Similarity 60.6%; Pred. No.3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tgaactacaagagacaaacaggtgactgcaagctgcccgaactgtgcccggagatc 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 237 tgaactctcaagaaactgataatgaacagtgagagctgccggcctgtgctacacatgca 296
QY 310 gaccctctcaacactatcccgtggccatccgcgtgtgactgagcgagctctccactgcc 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 297 gattccttgatatacattaccagtgccaccagtcactgtgtgcaagtgtgacagcgac 356
QY 370 accacgagatgt 381
    ||||| |||||
DB 357 agcactgattgt 368

```

```

RESULT 9
US-08-918-288-26
; Sequence 26, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

```

```

RESULT 10
US-09-282-357-26
; Sequence 26, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282.357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 33...700
OTHER INFORMATION:
US-09-282-357-26

Query Match      12.5%; Score 48.8; DB 4; Length 719;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tttacttaacagagacaacaaagtgtaactgtcaagctgtgcccaactgtgccccggagatc 309
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 tctaccttaacagaaactggtatgtgaaacagtgagagtgcccgctgtcctacacatgca 296
QY 310 gacccttctaacctatccgttgccatccgctgtgactgtggagagccctgcctccactgcc 369
    || ||||| ||| ||| ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
DB 297 gattccttctatatacattccacagtgccacccagtcactgtggcaagtgtagacagcgac 356
QY 370 accacggagtg 381
    | ||| ||| |||
DB 357 agcactgattgt 368

RESULT 11
US-08-918-288-11
; Sequence 11, Application US/08918288
; Patent No. 6238690
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
```

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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 33...719
OTHER INFORMATION:
US-08-918-288-11

Query Match      12.5%; Score 48.8; DB 4; Length 728;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tttacttaacagagacaacaaagtgtaactgtcaagctgtgcccaactgtgccccggagatc 309
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 tctaccttaacagaaactggtatgtgaaacagtgagagtgcccgctgtcctacacatgca 296
QY 310 gacccttctaacctatccgttgccatccgctgtgactgtggagagccctgcctccactgcc 369
    || ||||| ||| ||| ||| ||||| ||| ||||| ||| ||| ||| ||| ||| |||
DB 297 gattccttctatatacattccacagtgccacccagtcactgtggcaagtgtagacagcgac 356
QY 370 accacggagtg 381
    | ||| ||| |||
DB 357 agcactgattgt 368

RESULT 12
US-09-282-357-11
; Sequence 11, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
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? APPLICATION NUMBER: US/09/282,357
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/918,288
? FILING DATE: 25 AUG-1997
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 728 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: Coding Sequence
? LOCATION: 33...719
? OTHER INFORMATION:
? US-09-282-357-11

Query Match          12.5%; Score 48.8; DB 4; Length 728;
Best Local Similarity 60.6%; Pred. No. 3.9e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tgaacctacaagagacaaacaggtgactgtcaagctggcccaactgtgccccggagtc 309
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 237 tgaacctcaaaagaaactggtatgtgaaacagtgagtgcccgctgtctacacatgca 296

QY 310 gaccctctacacatcccggtggccatccgctgtgactgagcgagccttcacatgcc 369
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 297 gattccttgatracatracacacagtgccaccacagtgctgctggtgacagcgac 356

QY 370 accacgagatgt 381
    || ||| ||| |||
DB 357 agcactgattgt 368

RESULT 13
US-08-239-256-1
? Sequence 1, Application US/08239256
? Patent No. 5585345
? GENERAL INFORMATION:
? APPLICANT: BOIME, IRVING
? APPLICANT: MATZUK, MARTIN M.
? APPLICANT: KEENE, JEFFREY L.
? TITLE OF INVENTION: CTP EXTENDED FORM OF LH
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Ave. N.W.
? CITY: Washington, D.C.
? COUNTRY: USA
? ZIP: 20006-1812
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/239,256
? FILING DATE: 06-MAY-1994
? CLASSIFICATION: 435
```

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? ATTORNEY/AGENT INFORMATION:
? NAME: MURASHIGE, KATE H.
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20030.12
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? TELEX: 90-4030
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1006 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 238..396
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 292
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 461..686
? US-08-239-256-1

Query Match          12.5%; Score 48.8; DB 1; Length 1006;
Best Local Similarity 60.6%; Pred. No. 4.3e-05;
Matches 80; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 250 tgaacctacaagagacaaacaggtgactgtcaagctggcccaactgtgccccggagtc 309
    ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 506 tgaacctcaaaagaaactggtatgtgaaacagtgagtgcccgctgtctacacatgca 565

QY 310 gaccctctacacatcccggtggccatccgctgtgactgagcgagccttcacatgcc 369
    || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 566 gattccttgatracatracacacagtgccaccacagtgctgctggtgacagcgac 625

QY 370 accacgagatgt 381
    || ||| ||| |||
DB 626 agcactgattgt 637

RESULT 14
US-08-918-288-10/c
? Sequence 10, Application US/08918288
? Patent No. 6238890
? GENERAL INFORMATION:
? APPLICANT: BOIME, IRVING
? APPLICANT: MOYLE, WILLIAM R.
? TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
? APPLICATION NUMBER: 08/853,524
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